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Binomial analysis of proteogenomic data indicates enhanced ribosome architecture associated with high feed efficiency

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Global gene (microarray, RNA-Seq) and protein expression (shotgun proteomics) analyses have been conducted on the same set of breast muscle samples obtained from pedigree broiler (meat chicken) males exhibiting high and low feed efficiency (FE). Phenotyping for FE (g feed intake/g body weight gain) was conducted between 6 to 7 week of age on animals housed in individual cages. The FE for the high and low groups was 0.66+0.1 and 0.46+0.1, respectively. Using entire datasets (i.e. no cutoffs for P value or fold difference), we determined the number of genes or proteins that were expressed numerically higher in the high or low FE phenotypes for key terms; e.g., ribosomal, mitochondrial ribosomal, tRNA, RNA binding motif, RNA polymerase, small nuclear ribonucleoprotein, and nuclear transport proteins (karyopherins, importins, exportins). We then conducted binomial analysis on the numbers of molecules that had higher mean values (based on n=6 for microarray and RNA-Seq data and n=4 for shotgun proteomics) for each FE phenotype. Binomial analysis revealed a significant skew in all of these categories in the high FE compared to the low FE phenotype. These results suggest that processes of ribosomal construction, activity, and protein translation would be enhanced in high FE breast muscle. Interestingly, evidence of enhanced proteasomes and autophagy expression was also observed in high FE tissue which could indicate that repair processes were also enhanced in the high FE phenotype. These findings provide new insight into fundamental cellular mechanisms of feed efficiency.

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